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Isolation and characterization of *Bacillus anthracis* in Georgia from veterinary isolates

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Background: The Republic of Georgia, once a member of the former Soviet Union (FSU), is a country with a significant endemic pathogen population. Since investigation of these pathogens using modern methods has only just begun, there are many gaps in Georgia's current knowledge of the prevalence and incidence of certain priority pathogens, including the incidence of veterinary disease by *B. anthracis*.

Methods: In this study, we investigated through passive surveillance, the incidence of *B. anthracis* from suspect cases. During this project, a total of 127 samples were tested from soil and suspect animal infections for the identification of *Bacillus anthracis*. The testing algorithm included, Gram stain, lysis by Gamma phage, motility test, detection of poly-D-glutamic acid capsule by direct fluorescent antibody (DFA), detection of cell-wall associated polysaccharide by direct fluorescent antibody (DFA), malachite green staining, and PCR

Results: In total, 36 samples were confirmed positive for a *B. anthracis* infection. A total of 91 samples were negative with no other disease detected. A majority of the infected animal samples and positive results were from south/southeastern Georgia.

Conclusion: This research project supports disease surveillance in Georgia and significantly improves the country's public health system by enhancing surveillance, detection and research capabilities various *B. anthracis*.

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The overview of H5N1 highly pathogenic avian influenza virus strains isolated from migratory wild birds in Mongolia between 2005 and 2010

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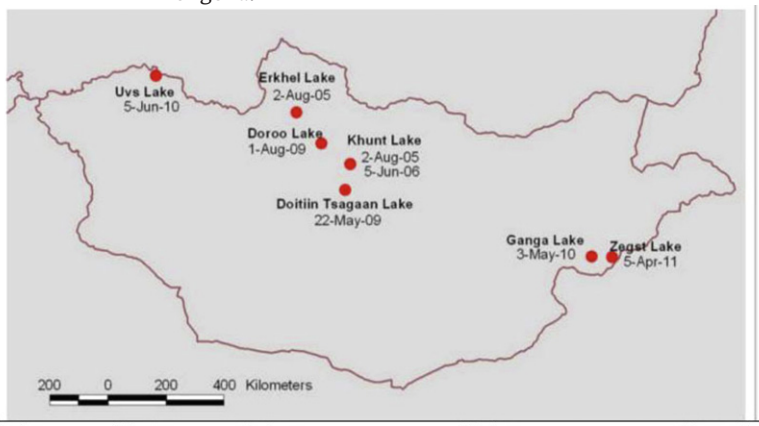
Background: The HPAI has become the most serious zoonotic problems in the world because of the concerns of the potential to cause human pandemic and currently 578 human cases confirmed infections have resulted in 340 deaths (2003-2011). In July 2005, May 2006, May 2009, July 2009, and May 2010, H5N1 HPAI viruses were isolated from whooper swans and other migratory wild birds in Mongolia.



Date	Place	Lake	Birds	Type of virus
5-Aug	Khuvsugul	Erkhel	Whooper swan, Bar-headed Goose	HPAIV-H5N1
5-Aug	Bulgan	Khunt	Whooper swan	HPAIV-H5N1
6-May	Bulgan	Khunt	Whooper swan	HPAIV-H5N1
6-May	Khuvsugul	Erkhel	Common goldeneye	HPAIV-H5N1
9-Aug	Arkhangai	Duruu	Bar-head goose, Common goldeneye, Ruddy shelduck	HPAIV-H5N1
9-May	Arkhangai	Doit	Whooper swan	HPAIV-H5N1
10-May	Sukhbaatar	Ganga	Whooper swan	HPAIV-H5N1

HPAI cases in Mongolia 2005-2010

Methods: Virus isolation was carried out from the homogenate of the brain, lungs, spleen of wild birds, which were found as carcasses in the Khunt, Erkhel, Doityn Tsagaan, Doroo and Ganga Lakes in Mongolia in July 2005, May 2006, May 2009, July 2009, and May 2010

Viruses isolated by the egg inoculation method, and RT-PCR, qRT-PCR and Neuraminidase inhibition test were used for subtyping.

The confirmation of the isolated HPAIV, and IVPI, phylogenetic analysis were performed by the OIE Reference Laboratory for HPAI at Hokkaido University, Japan.

Results: In July 2005, H5N1 viruses were isolated from tissue homogenates and swab samples of a bar-headed goose and a whooper swan in Khunt and Erkhel Lakes. Similarly, H5N1 viruses